

NA

1643

PAGE: 1

# RAW SEQUENCE LISTING

## PATENT APPLICATION US/09/428,122

 DATE: 02/24/2000  
 TIME: 16:25:32

Input Set: I428122.RAW

This Raw Listing contains the General Information  
 Section and up to first 5 pages.

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1 <110> APPLICANT: Connaught Laboratories Limited  
 2 Murdin et al.  
 3 <120> TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND  
 4 USES THEREOF  
 5 <130> FILE REFERENCE: 19721-007-019  
 6 <140> CURRENT APPLICATION NUMBER: US/09/428,122  
 7 <141> CURRENT FILING DATE: 1999-10-27  
 8 <150> EARLIER APPLICATION NUMBER: 60/106,046  
 9 <151> EARLIER FILING DATE: 1998-10-28  
 10 <150> EARLIER APPLICATION NUMBER: 60/132,271  
 11 <151> EARLIER FILING DATE: 1999-05-03  
 12 <160> NUMBER OF SEQ ID NOS: 4  
 13 <170> SOFTWARE: PatentIn Ver. 2.0  
 14 <210> SEQ ID NO 1  
 15 <211> LENGTH: 3000  
 16 <212> TYPE: DNA  
 17 <213> ORGANISM: Chlamydia pneumoniae  
 18 <220> FEATURE:  
 19 <221> NAME/KEY: CDS  
 20 <222> LOCATION: (101)..(2884)  
 21 <400> SEQUENCE: 1

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 24 Met Lys Ser Ser Phe  
 25 1 5  
 26 ccc aag ttt gta ttt tct aca ttt gct att ttc cct ttg tct atg att 163  
 27 Pro Lys Phe Val Phe Ser Thr Phe Ala Ile Phe Pro Leu Ser Met Ile  
 28 10 15 20  
 29 gct acc gag aca gtt ttg gat tca agt gcg agt ttc gat ggg aat aaa 211  
 30 Ala Thr Glu Thr Val Leu Asp Ser Ser Ala Ser Phe Asp Gly Asn Lys  
 31 25 30 35  
 32 aat ggt aat ttt tca gtt cgt gag agt cag gaa gat gct gga act acc 259  
 33 Asn Gly Asn Phe Ser Val Arg Glu Ser Gln Glu Asp Ala Gly Thr Thr  
 34 40 45 50  
 35 tac cta ttt aag gga aat gtc act cta gaa aat att cct gga aca ggc 307  
 36 Tyr Leu Phe Lys Gly Asn Val Thr Leu Glu Asn Ile Pro Gly Thr Gly  
 37 55 60 65  
 38 aca gca atc aca aaa agc tgt ttt aac aac act aag ggc gat ttg act 355  
 39 Thr Ala Ile Thr Lys Ser Cys Phe Asn Asn Thr Lys Gly Asp Leu Thr  
 40 70 75 80 85  
 41 ttc aca ggt aac ggg aac tct cta ttg ttc caa acg gtg gat gca ggg 403  
 42 Phe Thr Gly Asn Gly Asn Ser Leu Leu Phe Gln Thr Val Asp Ala Gly  
 43 90 95 100  
 44 act gta gca ggg gct gct gtt aac agc agc gtg gta gat aaa tct acc 451

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PAGE: 2

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56	gat aat ggc ggt gct atc acc gca aaa act ctt tca tta aca ggg act	643
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61		185 190 195
62	gcc att cag act tcc gat gcc ctt acc att act gga aac caa ggg gaa	739
63	Ala Ile Gln Thr Ser Asp Ala Leu Thr Ile Thr Gly Asn Gln Gly Glu	
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66	Val Ser Phe Ser Asp Asn Thr Ser Ser Asp Ser Gly Ala Ala Ile Phe	
67		215 220 225
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71	gac aat aag gtc aca gga gcg agc tcc tca aca acg ggg gat atg tca	883
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81	Ala Gly Gly Ala Ile Tyr Val Lys Lys Leu Glu Leu Ala Ser Gly Gly	
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83	ctt acc cta ttc agt aga aat agt gtc aat gga ggt aca gct cct aaa	1075
84	Leu Thr Leu Phe Ser Arg Asn Ser Val Asn Gly Gly Thr Ala Pro Lys	
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86	ggt gga gcc ata gct atc gaa gat agt ggg gaa ttg agt tta tcc gcc	1123
87	Gly Gly Ala Ile Ala Ile Glu Asp Ser Gly Glu Leu Ser Leu Ser Ala	
88		330 335 340
89	gat agt ggt gac att gtc ttt tta ggg aat aca gtc act tct act act	1171
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91		345 350 355
92	cct ggg acg aat aga agt agt atc gac tta gga acg agt gca aag atg	1219
93	Pro Gly Thr Asn Arg Ser Ser Ile Asp Leu Gly Thr Ser Ala Lys Met	
94		360 365 370

PAGE: 3

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/428,122

DATE: 02/24/2000  
TIME: 16:25:32

Input Set: I428122.RAW

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101	gag act ccg gca gat tct gca cta caa tat aca ggg aac atc atc ttc	1363
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103	410 415 420	
104	aca gga gaa aag tta tca gag aca gag gcc gca gat tct aaa aat ctt	1411
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106	425 430 435	
107	act tcg aag cta cta cag cct gta act ctt tca gga ggt act cta tct	1459
108	Thr Ser Lys Leu Leu Gln Pro Val Thr Leu Ser Gly Gly Thr Leu Ser	
109	440 445 450	
110	tta aaa cat gga gtg act ctg cag act cag gca ttc act caa cag gca	1507
111	Leu Lys His Gly Val Thr Leu Gln Thr Gln Ala Phe Thr Gln Gln Ala	
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117	Thr Ser Thr Ile Asn Asn Leu Val Ile Asn Ile Ser Ser Ile Asp Gly	
118	490 495 500	
119	gca aag aag gca aaa ata gaa acc aaa gct acg tca aaa aat ctg act	1651
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122	tta tct gga acc atc act tta ttg gac ccg acg ggc acg ttt tat gaa	1699
123	Leu Ser Gly Thr Ile Thr Leu Leu Asp Pro Thr Gly Thr Phe Tyr Glu	
124	520 525 530	
125	aat cat agt tta aga aat cct cag tcc tac gac atc tta gag ctc aaa	1747
126	Asn His Ser Leu Arg Asn Pro Gln Ser Tyr Asp Ile Leu Glu Leu Lys	
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128	gct tct gga act gta aca agc acc gca gtg act cca gat cct ata atg	1795
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132	Gly Glu Lys Phe His Tyr Gly Tyr Gln Gly Thr Trp Gly Pro Ile Val	
133	570 575 580	
134	tgg ggg aca ggg gct tct acg act gca acc ttc aac tgg act aaa act	1891
135	Trp Gly Thr Gly Ala Ser Thr Thr Ala Thr Phe Asn Trp Thr Lys Thr	
136	585 590 595	
137	ggc tat att cct aat ccc gag cgt atc ggc tct tta gtc cct aat agc	1939
138	Gly Tyr Ile Pro Asn Pro Glu Arg Ile Gly Ser Leu Val Pro Asn Ser	
139	600 605 610	
140	tta tgg aat gca ttt ata gat att agc tct ctc cat tat ctt atg gag	1987
141	Leu Trp Asn Ala Phe Ile Asp Ile Ser Ser Leu His Tyr Leu Met Glu	
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143	act gca aac gaa ggg ttg cag gga gac cgt gct ttt tgg tgt gct gga	2035
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PAGE: 4

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/428,122

DATE: 02/24/2000  
TIME: 16:25:32

Input Set: I428122.RAW

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149	cgc cat ttg agt ggc ggt	tat gtc ata gga gga	aac cta cat act tgt	2131				
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152	tca gat aag att ctt agt	gct gca ttt tgt cag	ctc ttt gga aga gat	2179				
153	Ser Asp Lys Ile Leu Ser	Ala Ala Phe Cys Gln	Leu Phe Gly Arg Asp					
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155	aga gac tac ttt gta gct	aag aat caa ggt aca	gtc tac gga gga act	2227				
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157		695	700	705				
158	ctc tat tac cag cac aac	gaa acc tat atc tct	ctt cct tgc aaa cta	2275				
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161	cgg cct tgt tgc ttg tct	tat gtt cct aca gag	att cct gtt ctc ttt	2323				
162	Arg Pro Cys Ser Leu Ser	Tyr Val Pro Thr Glu	Ile Pro Val Leu Phe					
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165	Ser Gly Asn Leu Ser Tyr	Thr His Thr Asp Asn	Asp Leu Lys Thr Lys					
166		745	750	755				
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168	Tyr Thr Thr Tyr Pro Thr	Val Lys Gly Ser Trp	Gly Asn Asp Ser Phe					
169		760	765	770				
170	gct tta gaa ttc ggt gga	aga gct ccg att tgc	tta gat gaa agt gct	2467				
171	Ala Leu Glu Phe Gly Gly	Arg Ala Pro Ile Cys	Leu Asp Glu Ser Ala					
172		775	780	785				
173	cta ttt gag cag tac atg	ccc ttc atg aaa ttg	cag ttt gtc tat gca	2515				
174	Leu Phe Glu Gln Tyr Met	Pro Phe Met Lys Leu	Gln Phe Val Tyr Ala					
175		790	795	800				
176	cat cag gaa ggt ttt aaa	gaa cag gga aca gaa	gct cgt gaa ttt gga	2563				
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178		810	815	820				
179	agt agc cgt ctt gtg aat	ctt gcc tta cct atc	ggg atc cga ttt gat	2611				
180	Ser Ser Arg Leu Val Asn	Leu Ala Leu Pro Ile	Gly Ile Arg Phe Asp					
181		825	830	835				
182	aag gaa tca gac tgc caa	gat gca acg tac aat	cta act ctt ggt tat	2659				
183	Lys Glu Ser Asp Cys Gln	Asp Ala Thr Tyr Asn	Leu Thr Leu Gly Tyr					
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186	Thr Val Asp Leu Val Arg	Ser Asn Pro Asp Cys	Thr Thr Thr Leu Arg					
187		855	860	865				
188	att agc ggt gat tct tgg	aaa acc ttc ggt acg	aat ttg gca aga caa	2755				
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190		870	875	880				
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PAGE: 5

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/428,122

DATE: 02/24/2000  
TIME: 16:25:32

Input Set: I428122.RAW

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198      Tyr Asn Val Asp Leu Gly Ala Lys Tyr Gln Phe
199                920                      925
200      agagctccat acatcgaagg gaaaagagct ttttaagattt cttgaaggct cttttcgatt 2964
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212                35          40          45
213      Asp Ala Gly Thr Thr Tyr Leu Phe Lys Gly Asn Val Thr Leu Glu Asn
214                50          55          60
215      Ile Pro Gly Thr Gly Thr Ala Ile Thr Lys Ser Cys Phe Asn Asn Thr
216                65          70          75          80
217      Lys Gly Asp Leu Thr Phe Thr Gly Asn Gly Asn Ser Leu Leu Phe Gln
218                85          90          95
219      Thr Val Asp Ala Gly Thr Val Ala Gly Ala Ala Val Asn Ser Ser Val
220                100         105         110
221      Val Asp Lys Ser Thr Thr Phe Ile Gly Phe Ser Ser Leu Ser Phe Ile
222                115         120         125
223      Ala Ser Pro Gly Ser Ser Ile Thr Thr Gly Lys Gly Ala Val Ser Cys
224                130         135         140
225      Ser Thr Gly Ser Leu Ser Leu Thr Lys Asn Val Ser Leu Leu Phe Ser
226                145         150         155         160
227      Lys Asn Phe Ser Thr Asp Asn Gly Gly Ala Ile Thr Ala Lys Thr Leu
228                165         170         175
229      Ser Leu Thr Gly Thr Thr Met Ser Ala Leu Phe Ser Glu Asn Thr Ser
230                180         185         190
231      Ser Lys Lys Gly Gly Ala Ile Gln Thr Ser Asp Ala Leu Thr Ile Thr
232                195         200         205
233      Gly Asn Gln Gly Glu Val Ser Phe Ser Asp Asn Thr Ser Ser Asp Ser
234                210         215         220
235      Gly Ala Ala Ile Phe Thr Glu Ala Ser Val Thr Ile Ser Asn Asn Ala
236                225         230         235         240
237      Lys Val Ser Phe Ile Asp Asn Lys Val Thr Gly Ala Ser Ser Ser Thr
238                245         250         255
239      Thr Gly Asp Met Ser Gly Gly Ala Ile Cys Ala Tyr Lys Thr Ser Thr
240                260         265         270
241      Asp Thr Lys Val Thr Leu Thr Gly Asn Gln Met Leu Leu Phe Ser Asn
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PAGE: 6

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PATENT APPLICATION US/09/428,122

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